

RAW SEQUENCE LISTING

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Application Serial Number: 10/552,515
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/552,515

DATE: 10/20/2005

TIME: 09:40:29

Input Set : A:\Sequence Listing.txt
 Output Set: N:\CRF4\10202005\J552515.raw

3 <110> APPLICANT: The Government of the United States of America as
 4 represented by the Secretary of the Department of Health and
 5 Human Services
 6 Bera, Tapan K.
 7 Pastan, Ira H.
 8 Lee, Byungkook
 10 <120> TITLE OF INVENTION: GENE EXPRESSED IN PROSTATE CANCER AND METHODS OF USE
 12 <130> FILE REFERENCE: 4239-68223-02
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/552,515
 C--> 14 <141> CURRENT FILING DATE: 2005-10-06
 14 <150> PRIOR APPLICATION NUMBER: PCT/US2004/10588
 15 <151> PRIOR FILING DATE: 2004-04-05
 17 <150> PRIOR APPLICATION NUMBER: 60/461,399
 18 <151> PRIOR FILING DATE: 2003-04-08
 20 <160> NUMBER OF SEQ ID NOS: 12
 22 <170> SOFTWARE: PatentIn version 3.2
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 933
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
 32 <400> SEQUENCE: 1
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 35 1 5 10 15
 38 Pro Thr Leu Cys Pro Ala Val Arg Thr Gly Leu Tyr Cys Arg Asp Gln
 39 20 25 30
 42 Ala His Ala Glu Arg Trp Ala Met Thr Ser Glu Thr Ser Ser Gly Ser
 43 35 40 45
 46 His Cys Ala Arg Ser Arg Met Leu Arg Arg Arg Ala Gln Glu Glu Asp
 47 50 55 60
 50 Ser Thr Val Leu Ile Asp Val Ser Pro Pro Glu Ala Glu Lys Arg Gly
 51 65 70 75 80
 54 Ser Tyr Gly Ser Thr Ala His Ala Ser Glu Pro Gly Gly Gln Gln Ala
 55 85 90 95
 58 Ala Ala Cys Arg Ala Gly Ser Pro Ala Lys Pro Arg Ile Ala Asp Phe
 59 100 105 110
 62 Val Leu Val Trp Glu Glu Asp Leu Lys Leu Asp Arg Gln Gln Asp Ser
 63 115 120 125
 66 Ala Ala Arg Asp Arg Thr Asp Met His Arg Thr Trp Arg Glu Thr Phe
 67 130 135 140
 70 Leu Asp Asn Leu Arg Ala Ala Gly Leu Cys Val Asp Gln Gln Asp Val
 71 145 150 155 160

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75 165 170 175
78 Ala Val Leu Cys Tyr Tyr Ala Glu Asp Leu Arg Leu Lys Leu Pro Leu
79 180 185 190
82 Gln Glu Leu Pro Asn Gln Ala Ser Asn Trp Ser Ala Gly Leu Leu Ala
83 195 200 205
86 Trp Leu Gly Ile Pro Asn Val Leu Leu Glu Val Val Pro Asp Val Pro
87 210 215 220
90 Pro Glu Tyr Tyr Ser Cys Arg Phe Arg Val Asn Lys Leu Pro Arg Phe
91 225 230 235 240
94 Leu Gly Ser Asp Asn Gln Asp Thr Phe Phe Thr Ser Thr Lys Arg His
95 245 250 255
98 Gln Ile Leu Phe Glu Ile Leu Ala Lys Thr Pro Tyr Gly His Glu Lys
99 260 265 270
102 Lys Asn Leu Leu Gly Ile His Gln Leu Leu Ala Glu Gly Val Leu Ser
103 275 280 285
106 Ala Ala Phe Pro Leu His Asp Gly Pro Phe Lys Thr Pro Pro Glu Gly
107 290 295 300
110 Pro Gln Ala Pro Arg Leu Asn Gln Arg Gln Val Leu Phe Gln His Trp
111 305 310 315 320
114 Ala Arg Trp Gly Lys Trp Asn Lys Tyr Gln Pro Leu Asp His Val Arg
115 325 330 335
118 Arg Tyr Phe Gly Glu Lys Val Ala Leu Tyr Phe Ala Trp Leu Gly Phe
119 340 345 350
122 Tyr Thr Gly Trp Leu Leu Pro Ala Ala Val Val Gly Thr Leu Val Phe
123 355 360 365
126 Leu Val Gly Cys Phe Leu Val Phe Ser Asp Ile Pro Thr Gln Glu Leu
127 370 375 380
130 Cys Gly Ser Lys Asp Ser Phe Glu Met Cys Pro Leu Cys Leu Asp Cys
131 385 390 395 400
134 Pro Phe Trp Leu Leu Ser Ser Ala Cys Ala Leu Ala Gln Ala Gly Arg
135 405 410 415
138 Leu Phe Asp His Gly Gly Thr Val Phe Phe Ser Leu Phe Met Ala Leu
139 420 425 430
142 Trp Ala Val Leu Leu Glu Tyr Trp Lys Arg Lys Ser Ala Thr Leu
143 435 440 445
146 Ala Tyr Arg Trp Asp Cys Ser Asp Tyr Glu Asp Thr Glu Glu Arg Pro
147 450 455 460
150 Arg Pro Gln Phe Ala Ala Ser Ala Pro Met Thr Ala Pro Asn Pro Ile
151 465 470 475 480
154 Thr Gly Glu Asp Glu Pro Tyr Phe Pro Glu Arg Ser Arg Ala Arg Arg
155 485 490 495
158 Met Leu Ala Gly Ser Val Val Ile Val Val Met Val Ala Val Val Val
159 500 505 510
162 Met Cys Leu Val Ser Ile Ile Leu Tyr Arg Ala Ile Met Ala Ile Val
163 515 520 525
166 Val Ser Arg Ser Gly Asn Thr Leu Leu Ala Ala Trp Ala Ser Arg Ile
167 530 535 540
170 Ala Ser Leu Thr Gly Ser Val Val Asn Leu Val Phe Ile Leu Ile Leu

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171	545	550	555	560
174	Ser Lys Ile Tyr Val Ser Leu Ala His Val	Leu Thr Arg Trp Glu Met		
175	565	570	575	
178	His Arg Thr Gln Thr Lys Phe Glu Asp Ala Phe	Thr Leu Lys Val Phe		
179	580	585	590	
182	Ile Phe Gln Phe Val Asn Phe Tyr Ser Ser Pro Val	Tyr Ile Ala Phe		
183	595	600	605	
186	Phe Lys Gly Arg Phe Val Gly Tyr Pro Gly Asn Tyr	His Thr Leu Phe		
187	610	615	620	
190	Gly Val Arg Asn Glu Glu Cys Ala Ala Gly Gly	Cys Leu Ile Glu Leu		
191	625	630	635	640
194	Ala Gln Glu Leu Leu Val Ile Met Val Gly Lys Gln	Val Ile Asn Asn		
195	645	650	655	
198	Met Gln Glu Val Leu Ile Pro Lys Leu Lys Gly Trp	Trp Gln Lys Phe		
199	660	665	670	
202	Arg Leu Arg Ser Lys Lys Arg Lys Ala Gly Ala Ser	Ala Gly Ala Ser		
203	675	680	685	
206	Gln Gly Pro Trp Glu Asp Asp Tyr Glu Leu Val Pro	Cys Glu Gly Leu		
207	690	695	700	
210	Phe Asp Glu Tyr Leu Glu Met Val Leu Gln Phe	Gly Phe Val Thr Ile		
211	705	710	715	720
214	Phe Val Ala Ala Cys Pro Leu Ala Pro Leu Phe	Ala Leu Leu Asn Asn		
215	725	730	735	
218	Trp Val Glu Ile Arg Leu Asp Ala Arg Lys Phe	Val Cys Glu Tyr Arg		
219	740	745	750	
222	Arg Pro Val Ala Glu Arg Ala Gln Asp Ile Gly	Ile Trp Phe His Ile		
223	755	760	765	
226	Leu Ala Gly Leu Thr His Leu Ala Val Ile Ser Asn	Ala Phe Leu Leu		
227	770	775	780	
230	Ala Phe Ser Ser Asp Phe Leu Pro Arg Ala Tyr	Tyr Arg Trp Thr Arg		
231	785	790	795	800
234	Ala His Asp Leu Arg Gly Phe Leu Asn Phe	Thr Leu Ala Arg Ala Pro		
235	805	810	815	
238	Ser Ser Phe Ala Ala Ala His Asn Arg Thr Cys	Arg Tyr Ala Phe		
239	820	825	830	
242	Arg Asp Asp Asp Gly His Tyr Ser Gln Thr Tyr	Trp Asn Leu Leu Ala		
243	835	840	845	
246	Ile Arg Leu Ala Phe Val Ile Val Phe Glu His	Val Val Phe Ser Val		
247	850	855	860	
250	Gly Arg Leu Leu Asp Leu Leu Val Pro Asp Ile	Pro Glu Ser Val Glu		
251	865	870	875	880
254	Ile Lys Val Lys Arg Glu Tyr Tyr Leu Ala Lys	Gln Ala Leu Ala Glu		
255	885	890	895	
258	Asn Glu Val Leu Phe Gly Thr Asn Gly Thr Lys	Asp Glu Gln Pro Lys		
259	900	905	910	
262	Gly Ser Glu Leu Ser Ser His Trp Thr Pro Phe	Thr Val Pro Lys Ala		
263	915	920	925	
266	Ser Gln Leu Gln Gln			
267	930			

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Input Set : A:\Sequence Listing.txt
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270 <210> SEQ ID NO: 2
 271 <211> LENGTH: 3308
 272 <212> TYPE: DNA
 273 <213> ORGANISM: Artificial Sequence
 275 <220> FEATURE:
 276 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
 278 <400> SEQUENCE: 2
 279 aaaagataga tcctgctcca ggagccggga agcctcgccc tggccagctg tgctgggcac 60
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 283 ctgcctgggc ggggtccaa gggccacccc tccccaccct ctgtcccgca gtgaggacgg 180
 285 gactctactg ccgagaccag gtcacacgtg agaggtggc catgacacctt gagacacttt 240
 287 ccggaaagcca ctgtgccagg agcaggatgc tgcggcgcacg ggcccaggaa gaggacagca 300
 289 ccgtccctgat cgatgtgagc cccccctgagg cagagaagag gggctttag cggagcacag 360
 291 cccacgcctc ggagccagggt ggacagcaag cggccgcctg cagagctgg agtccctgcca 420
 293 agccccggat cgcagacttc gtccctcggtt gggaggagga cctgaagcta gacaggcagc 480
 295 aggacagtgc cgccccggac agaacagaca tgcacaggac ctggcgggag acttttctgg 540
 297 ataatctcg tgcggctggg ctgtgtgttag accagcagga cgtccaggac gggAACACCCA 600
 299 cagtgcacta cgccttcctc agcgcctctt gggctgtgtct ctgtactac gccgaagacc 660
 301 tgcgcctgaa gtcgccttg caggagttac ccaaccaggc ctccaaactgg tcggccggcc 720
 303 tgctggcatg gctggcattc cccaaacgtcc tgctggaggt tgcgccttgc acgttgcac 780
 305 agtactactc ctgcgggttc agagtgaaca agtgcacacg cttccctcggt agtacaacc 840
 307 aggacacactt ctgcacaaggc accaagaggc accaaattct gtttgagatc ctggccaaga 900
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 311 tgcgccttcc ctgcatacg gccccttcaa gacgccccca gagggccccgc 1020
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 315 ggaacaagta ccagccccctg gaccacgtgc gcaggtactt cggggagaag gtggccctct 1140
 317 acttcgcctg gctcggttt tacacaggtt ggctcctgccc agcggcagtg gtgggcacac 1200
 319 tgggtttccct ggtggctgc ttccctgggt ttcagacat acccacgcac gaactgtgtg 1260
 321 gcagcaagga cagcttcgag atgtgcacccat tttgcctcgat ctggcccttc tggctgtct 1320
 323 ccagcgctg tgcctggcc caggccggcc ggctttcgat ccacggccgc accgtgttct 1380
 325 tcagcttgtt catggcaactg tggccgtgc tgctgtgtt gtaactggaa cgaaagagcg 1440
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 329 cccagttgc cgccttgc cccatgacag ccccaaccc catcacgggt gaggacgagc 1560
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 335 ccatcggtt gtccaggatcg ggcaacaccc ttctcgacgc ctggccctct cgcacatcgcca 1740
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 341 ctttcacccat caagggtttc atcttcacgt tgcgtcaactt ctactccat cccgtctaca 1920
 343 ttgccttctt caagggtggg acccaggcaat ctaccacacc ttgtttggag 1980
 345 tccgcaatga ggagtgcgcg gctggaggtt gctgtatcgat gctggcacag gagctctgg 2040
 347 tcatcatgtt gggcaagcag gtcataaca acatgcagga ggtcctcatc ccgaagctaa 2100
 349 agggctgggt gcagaaggatcc cggcttcgtt ccaagaagag gaaggcggtt gcttctgcag 2160
 351 gggctagcca gggccctgg gaggacgact atgagctgtt gccctgtgag ggtctgttt 2220
 353 acgacttccat ggaaatgggtt ctgcgttccat gcttcgtatc catcttcgtt gccgcctgtc 2280
 355 cgttcgtgc gcttcgtcc ctgctcaaca actgggtggat gatccgttgc gacgcgcgc 2340
 357 agtctgtctg cgagtaccgg cgcctgtgg cggagcgcgc ccaggacatc ggcacatgtt 2400
 359 tccacatctt cgcggccctc acgcacatcg cggatcatcg caacgccttc ctctggct 2460
 361 ttcgtccat cttccatcg cgcgcctact accgggtggac ccgcgcac gacatcgccg 2520

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363 gttcctcaa cttcacgctg ggcgagccc cgtcctcatt cgccgcccgg cacaaccgca 2580
365 cgtcaggta tcgggcttgc cggatgacg atggacatta ttcccagacc tactggaatc 2640
367 ttcttgccat ccgcctggcc ttcgtcattt tggtttagca tgggttttc tccgttggcc 2700
369 gcctcctggaa cctcctgggt cctgacatcc cagagtctgt ggagatcaaa gtgaagcgaa 2760
371 agtactacct ggctaagcag gcaactggctg agaatgaggt tctttttggaa acgaacggaa 2820
373 caaaggatgaa gcagccccaa ggctcagagc tcagctccca ctggacacccc ttcacgggtc 2880
375 ccaaggccaa ccagctgcag cagtgcacggc tggaggaca tctgggtggtc ctttagggag 2940
377 tggccctcc tgagccctgc gagcagcggtc ctttcctct tccctcaggc agggctgtg 3000
379 tgaaccgctg gctgctgttgc tgcctcatct ctgggcacat tgcctgttgc ccccccggc 3060
381 cggcttcctc cctcagagcgc cctgtcactc catccccggc agggaggac cgtcagctca 3120
383 caaggccctc ttgtttccct gctcccagac ataagccaa gggggccctg caccgaagg 3180
385 accctgtccc tcgggtggccct ccccaggccc ctggacacgaa cagttcttccct caggcagggtg 3240
387 ggcttgggg tcctcggccac ccctggccac atcgcctctt ccttttacac ctggtgaccc 3300
389 tcgaatgt 3308

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394 <212> TYPE: PRT
395 <213> ORGANISM: Artificial Sequence
397 <220> FEATURE:
398 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
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403 1 5
406 <210> SEQ ID NO: 4
407 <211> LENGTH: 9
408 <212> TYPE: PRT
409 <213> ORGANISM: Artificial Sequence
411 <220> FEATURE:
412 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
414 <400> SEQUENCE: 4
416 Val Leu Leu Glu Val Val Pro Asp Val
417 1 5
420 <210> SEQ ID NO: 5
421 <211> LENGTH: 9
422 <212> TYPE: PRT
423 <213> ORGANISM: Artificial Sequence
425 <220> FEATURE:
426 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
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431 1 5
434 <210> SEQ ID NO: 6
435 <211> LENGTH: 9
436 <212> TYPE: PRT
437 <213> ORGANISM: Artificial Sequence
439 <220> FEATURE:
440 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
442 <400> SEQUENCE: 6
444 Leu Leu Ala Ile Arg Leu Ala Phe Val
  
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/552,515

DATE: 10/20/2005

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Input Set : A:\Sequence Listing.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date